CABIOS ANNUAL AUTHOR INDEX

Allison,L. 1
Argos,P. 25,49,59
Arnold,J. 201,215
Arrigo,P. 687
Asai,K. 141
Asano,C. 375
Aszódi,A. 523
Aten,J.A. 381
Athanasiadis,A.D. 325
Attimonelli,M. 541

Balcão,V.M. 629
Balzarotti,V. 93
Barrai,I. 647
Barton,G.J. 729,745
Bellon,P.L. 681
Bolshoy,A. 435
Bordo,D. 639
Bork,P. 183
Brown,J.W. 465,473
Bucke,C. 723

Camussi,A. 695
Cardo,P.P. 687
Castañera,P. 535
Chao,K.-M. 387
Chau,F.T. 531
Chen,E.S. 375
Clarkson,M.I. 597
Cockcroft,V.B. 741
Cohen,B.I. 373
Cohen,F.E. 373
Cohen,M.I. 475
Colizzi,V. 93
Collins,D.W. 337
Cooley,R.E. 657
Cremer,C. 381
Cuticchia,A.J. 201,215

D'Orazio,T. 701
Damiani,G. 687
Danchin,A. 315
Date,S. 397
Davison,D.B. 375
Day,W.H.E. 653
De Rijk,P. 735
De Wachter,R. 177,735
Delahunty,M.D. 127
Deléage,G. 87,197
Deplanque,S. 667
Dibdin,G.H. 109
Distante,A. 701
Dohi,H. 459
Dopazo,J. 101,123,535

Edwards,M. 657
Eroshkin,A.M. 491
Etienne,A. 551
Etzold,T. 49,59

Fagin,B. 221
Ferrán,E.A. 671
Florence,L.Z. 517
Fomin,V.I. 491
Fuchs,R. 71,587,760
Fumoto,M. 243
Furuichi,E. 259

Gaboriaud,C. 37
Gaspin,Ch. 551
Geourgon,C. 87,197
Giuliano,F. 687
Gotoh,O. 361
Grau,E. 275
Green,D.K. 593
Gross,R. 221
Grune,T. 573

Handa,K. 141
Harauz,G. 472
Hardison,R.C. 387
Harrington,M.G 133
Hatzopoulos,A.A. 325
Hauer-Jensen,M. 45
Hausmann,M. 381
Hayamizu,S. 141
Hedman,F. 117
Hegyi,H. 371
Heijne,G.von 117
Heilig,R. 381
Hénaut,A. 191,315
Henneke,C.M. 709
Henrissat,B. 37
Hirosawa,M. 161
Holzhütter,H.-G. 573
Hoshida,M. 161,267
Howard,A. 413
Huang,W.-X. 475
Hunter,P.R. 403

Ikeda,J.-E. 343,349
Ischenko,I.V. 617
Ishikawa,M. 161,267
Ishizuka,M. 459

Jurka,J. 407

Kanehisa,M. 153,267
Karasawa,T. 243
Kel,A.E. 617
Kiong,B.-K. 211,581
Kleffe,J. 275
Kolaskar,A.S. 397
Kolchanov,N.A. 617
Kozlov.N.N. 253
Krishna,D. 29
Kugushev,E.I. 253
Kuhara,S. 259
Kulkarni,B. 397
Kulkarni,R. 397
Kulkarni-Kale,U. 397
Kypr,J. 355

Landès,C. 191
Landini,G. 547
Lanzavecchia,S. 681
Lavaitte,S. 37
Lefèvre,C. 343,349
Lemesle-Varloot,L. 37
Lestang,F. 37
Likhachev,E.A. 617
Liuni,S. 541,701
Livingstone,C.D. 745
Lunt,G.G. 741
Lüttke,A. 760

Mack,J.P.G. 127
McMorris,F.R. 653
Makarova,K.S. 17
Maksyutov,A.Z. 291
Malcata,F.X. 629
Marr,T.G. 499
Matsuo,Y. 153
Mehldau,G. 299
Mendes,P. 563
Milanesi,L. 617
Miller,W. 169,387
Milosavljević,A. 407
Minoshima,S. 459
Mitra,C.K. 227
Morante,S. 93
Morgat,A. 37
Mornon,J.-P. 37,667
Moya,A. 101
Mrázek,J. 355
Mujumdar,M.P. 227
Muller,G. 551
Myers,G. 299

Nash,J.H.E. 469
Nedde,D.N. 331
Nešović,Ž. 472
Nichols,B.E. 757
Nishioka,T. 9
Nitta,K. 267

O'Hara,P.J. 65
Oda,J. 9
Ogiwara,A. 9,267
Orlov,Y.L. 617
Ortells,M.O. 741

Pandey,A.C. 477
Panjukov,V.V. 285
Pantel,G. 37
Parisi,V. 93
Partner,P.L.R. 597
Pesole,G. 541,701
Petrilli,P. 205
Pflugfelder,B. 671
Pongor,S. 371
Ponomarenko,M.P. 617
Portugal,J. 607
Presnell,S.R. 373
Prestridge,D.S. 113
Prior,M.G. 517
Prunella,N. 541,701

Quedenau,J. 573

Rastall,R.A. 723
Reddy,P.J. 29
Rens,W. 381
Rippin,J.W. 547
Risler,J.-L. 191
Rodríguez,A. 123
Rodriguez-Larralde,A. 647
Rohde,K. 183
Rouxel,T. 315

Sáiz,J.C. 123
Sakaki,Y. 427
Sakamoto,N. 427
Salas,X. 607
Sasagawa,F. 147
Satou,K. 259
Sauro,H.M. 441
Scalia,F. 687
Scapoli,C. 647
Schuster,R 79
Schuster,S. 79
Schwendel,A. 573
Searls,D.B. 421
See,W.R. 475
Semertzidis,M.T. 667
Sheffield,V.C. 757
Shifman,M.A. 511
Shimizu,N. 459
Shpigelman,E.S. 435
Siems,W. 573
Silvestre,E. 535
Smith,J.M. 479
Smith,M.L. 597
Smutzer,G. 474
Sobrino,F. 123
Solomon,J.E. 133
Solovyev,V.V. 17
Spoor,W. 597
Stefanini,F.M. 695
Stella,E. 701
Stoehr,P. 71
Stone,E.M. 757
Stormo,G. 113
Suryanarayana,M.V.S. 477
Suyama,M. 9
Sykes,J.T. 723

Taberner,A. 101,535
Tabuchi,K. 243
Tajima,K. 147
Takagi,T. 259,427
Takiguchi,K. 259
Tan,T.-W. 211,581
Taylor,S.J.E. 723
Taylor,W.R. 523
Theophilidis,G. 325
Timberlake,W.E. 201,215
Tosoni,L. 681
Toya,T. 161,267
Trifonov,E.N. 435
Trubuil,A. 451

Van de Peer,Y. 177
Venezia,D. 65
Vishwakarma,R.K. 477
Vogt,G. 25
Volinia,S. 647

Wallin,E. 117
Ward,M.O. 331
Watt,J.G. 221
Westhof,E. 551
Wettergren,C. 117
Winter,S.C. 723

Yan,K.C. 531
Yasukawa,T. 243
Yee,C.N. 1
Yee,D. 517

Zagrebelnaya,E.S. 291
Zhang,M.Q. 499
Zhilkin,P.A. 491

ANNUAL SUBJECT INDEX

ADEPT
protein antigenic determinants prediction 291
AMAS
protein sequence alignment 745
Amino acid
oligonucleotide primer design 469
sequence motif analysis, database 9
Amino acid sequence
oligopeptide homology, molecular mimicry 93
ANREP
sequence analysis, pattern matching 299
ANTHEPROT
protein secondary structure software package 197
sequence analysis 87
APLOGEN
genetic algorithm, Monte Carlo simulation 695
ATPase
electrogenic property, computer simulation 227
Autoimmune disease
molecular mimicry 93
BASIC
experimental design 629
lethal dose estimation, LD50.BAS 477
logit transformations, biocide dosage 29
Binding constants
curve fitting, spreadsheet 127
Biochemical engineering
experimental design, STADEERS 629
Biochemistry
modelling reaction networks, GEPASI 563
reaction system, flux rate, intermediary metabolism 79
Biocide dosage
logit transformations, BASIC 29
Biocomputing
retrieval software, network information, HYBROW 581
BlockSearch
protein block searches, VAX/Alpha 587
BPTI
protein folding simulation model 243
Carbohydrate
sequence analysis, representation techniques 723
CD-ROM
sequence databank query system, EMBL-Search 71
CEDIT
protein sequence alignment, editing, Microsoft Word 741
Chromosome profile
slit-scan flow cytometry 381
Computer simulation
electrogenic property of ATPase 227
Connection Machine
parallel alignment of DNA sequence 375
Connection topology
protein 523
CONSENSUS
consensus sequence analysis, CONSENSUS 653
Consensus sequence
plurality rule, CONSENSUS 653
Contig mapping
PCAB 201
Correlation image
sequence analysis, nucleic acids 331
Crop selection
simulation 597
CURVATURE
curved DNA structure analysis 435
Curve fitting
error analysis, spreadsheet 127
Cyanobacteria
bloom simulation, SCUM 413
Data-acquisition
muscle, isometric tension, IBM-PC 325
Databank
protein structure, OMEGA 667
Database
amino acid sequence motif, Enzyme–Reaction Database 9
file handling, nucleotide 474
flat file retrieval tool, SRS 49
human genome, oligonucleotide, ODS 427
metabolic pathways, METALGEN.DB 315
protein structure analysis, PACADE 259
transcription factor binding site, SIGNAL SCAN 3.0 113
DCSE
nucleotide sequence alignment, secondary structure 735
Diffusion cell study
sampling-volume errors 109
DNA
gel electrophoresis PFGE MAPPER
sequence analysis, pattern recognition, DNA-Lexemics 349
sequence search, FASTPAT 541
structure analysis, CURVATURE 435
DNA sequence
algorithmic significance 407
analysis, SIMD, WORDUP 701
mapping algorithm, ODS 215
parallel alignment, Connection Machine 375
DOCMA
Dot-plot comparisons, protein sequence classification 191
Dot-plot comparisons
protein sequence classification, multivariate analysis, DOCMA 191
3DVISION
RNA structure 3-D modelling, PC 472
Dynamic programming
multiple sequence alignment, MASCOT 161
Electron microscopy
Fourier analysis, UNIX 681
Electrophoresis
one-dimensional, electrophoregram analysis, XE1D 451
PC control of 593
Electrophoresis gels
automation of protein detection 133
EMBL-Search
sequence databank query system, CD-ROM 71
ENVIRON
protein sequence alignment, 3-D structure 639
Enzyme–Reaction Database
amino acid sequence motif analysis 9
Enzymology
computer simulation 227
Error analysis
curve fitting, spreadsheet 127
Evolution
macromolecules, string alignment algorithm 1
phylogeny, RNA sequence Macintosh Hypercard 473
Evolutionary trees
construction of, software package, TREECON 177
Experimental design
biochemical engineering, STADEERS 629
Expert systems
knowledge acquisition 657
FASTA search
domain homology, SWISS-PROT, FTHOM 371
FASTPAT

DNA sequence search 541
FISH
coding sequence analysis, GenBank 337
Flat file
cross-referencing library, sequence database 59
database retrieval tool, SRS 49
Flux rate
reaction system, biochemistry 79
Folding
simulation, tRNA 253
Footprinting
DNA sequence analysis, DNA-Lexemics 349
quantitative analysis, PERFILS 607
Fourier analysis
3-D reconstruction, electron microscopy, FT3D 681
Fractal
dimension estimation using the mass–radius method 547
FT3D
Fourier analysis, UNIX 681
FTHOM
FASTA search, SWISS-PROT 371
GCG package
hypertext-like system for sequence analysis, HYGCG 211
Gel electrophoresis
pulsed field, PFGE MAPPER 511
GenBank
coding sequence analysis, FISH 337
Gene
special purpose computer processor, sequence analysis 221
Gene mapping
graphical user interface, GeneView 459
Genetic algorithm
object-oriented programming, APLOGEN 695
Genetic distance
autigenic reactivity, vaccine design 101
GeneView
gene mapping library, X-window 459
Genome
primer design, PCR amplification 123
GEPASI
modelling of reaction networks 563
Graphical analysis
image scanning, SCANGRAPH 531
Graphical representation
protein connection topology 523
Graphics
circular dichroism spectrum, software package, ANTHEPROT 197
display of RNA secondary structure 551
neurophysiology, screen-dump 475
Greek key
jellyroll, protein structure 709
GROUP REP
strain typing, microbial isolates 403
Growth prediction
modelling using a neural network 517
GSP
gene sequence analysis, special purpose computer processor 221
Homology
FASTA search, FTHOM 371
protein sequence classification 205
Human genome
oligonucleotide database, sequence analysis 427
HYBROW
biocomputing retrieval software, network information, UNIX interface 581
HYGCG
hypertext-like system for sequence analysis 211
Hypercard interface
human linkage analysis 757
Hypertext
network information retrieval software, HYBROW 581
Hypertext-like system
sequence analysis, HYGCG 211
IBM-PC
data-acquisition, isometric tension 325
Image scanning
TIFF file, SCANGRAPH 531
Intermediary metabolism
reaction system flux rate 79
Jellyroll
protein structure 709
Knowledge acquisition
expert systems 657
Kohonen's map
nucleic acid analysis 687
Lethal dose
estimation, up-and-down method, LD50.BAS 477
Linkage analysis
Hypercard interface 757
Logit transformations
BASIC 29
Macintosh Hypercard
RNA sequence, phylogeny 473
MacMatch
protein secondary structure prediction 373
MacP12
protein sequence property, multi-profile plot 760
MAKPAT
protein sequence analysis, pattern-matching 183
Malthusian parameter
population growth, rate of natural increase 535
MANSEK
protein sequence, hydrophobic cluster analysis 37
Mapping algorithm
DNA sequence ordering, ODS 215
Markov model
protein secondary structure prediction 141
MASCOT
multiple protein sequence alignment, dynamic programming 161
Mass–radius method
fractal dimension estimation 547
Metabolic pathway
analysis and simulation, SCAMP 441
Metabolic systems
simulation, flux rate estimation 573
Metabolism
graphics-oriented database, METALGEN.DB 315
METALGEN.DB
metabolic pathways, graphics-oriented database 315
Microbial isolates
strain typing, GROUP REP 403
Modelling
biochemistry, GEPASI 563
using a neural network 517
Molecular mimicry
amino acid sequence analysis, oligopeptide homology 93
Monoclonal antibodies
autigenic reactivity, genetic distance, vaccine design 101
Monte Carlo simulation
genetic algorithm, APLOGEN 695
MOTIF
match weight sets, sequence analysis 65
Motif compliance
sequence analysis, MOTIF 65

Motif scanning
ANTHEPROT 87
Multi-profile plot
protein sequence property 760
Multiple alignment
ANTHEPROT 87
Muscle
isometric tension, IBM-PC 325
Needleman–Wunsch
sequence databank, parallel computer 117
Network
flat file library network 59
Network information
hypertext, HYBROW 581
Neural network
growth prediction modelling 517
protein secondary structure prediction 147
Neural networks
nucleic acid analysis 687
protein sequence clustering 671
Neurophysiology
graphics screen-dump 475
Nucleic acid
functional sites analysis, Kohonen's map, neural networks 687
sequence, splice site analysis, SITEVIDEO 617
Nucleic acids
sequence analysis, correlation image 331
Nucleotide
database file handling 474
sequence alignment, DCSE 735
Object-oriented programming
genetic algorithm, APLOGEN 695
ODS
DNA sequence ordering, mapping algorithm 215
OLIGOGET
computerized oligonucleotide database 479
Oligonucleotide
computerized database, OLIGOGET 479
database, signal sequence analysis, ODS 427
primer design, amino acid sequence 469
probe choice, PCAB 201
transcription control, vertebrate 647
Oligopeptide frequency
protein sequence oligopeptide frequency, functional sites, domain localization 17
Oligopeptide homology
molecular mimicry, amino acid sequence analysis 93
OMEGA
protein structure databank 667
PACADE
protein structure analysis, database 259
Parallel alignment
DNA sequence, Connection Machine 375
Parallel computer
multiple sequence alignment, C-DAC 397
Needleman–Wunsch scanning of sequence databank 117
protein sequence homology, Profilesearch 25
Parallel computing
DNA sequence analysis 701
Pattern
DNA sequence, algorithmic significance 407
Pattern distribution
random sequence, JOINTD 275
Pattern matching
sequence analysis, ANREP 299
PC
RNA structure 3-D modelling 472
slit-scan flow cytometry, chromosome profile 381
PC control
pulsed-field electrophoresis 593
PCAB
sequence analysis, oligonucleotide probe choice, contig mapping 201
PCR amplification
primer design, variable genome 123
Pearl necklace model
protein folding simulation model 243
PERFILS
quantitative analysis of footprinting 607
PESTry
sequence analysis, word recognition 343
PFGE MAPPER
pulsed field gel electrophoresis 511
Phylogeny
evolution, Macintosh Hypercard 473
Plurality rule
consensus sequence analysis 653
Population growth
rate of natural increase 535
PostScript
sequence analysis, RSVP 421
Primer design
oligonucleotide, amino acid 469
PCR amplification variable genome 123
ProAnal
protein structure-activity relationship, sequence alignment 491
Profilesearch
protein sequence homology, parallel computer 25
PROPATS
protein sequence analysis, pattern-matching 183
Protein
antigenic determinants prediction, ADEPT 291
connection topology, graphical representation 523
detection of structural motifs 153
optimal sequence alignment 729
pattern-matching, MAKPAT, PROPATS 183
secondary structure, graphics software package 197
secondary structure prediction, MacMatch 373
secondary structure prediction, Markov model 141
secondary structure prediction, neural network 147
sequence alignment, CEDIT 741
sequence alignment, MASCOT 161
sequence alignment, residue conservation, AMAS 745
sequence alignment, structure-activity relationship 491
sequence analysis, block searches, BlockSearch 587
sequence classification, DOCMA 191
sequence classification, homology 205
structural motifs, 3-D structure, ENVIRON 639
structure analysis, PACADE 259
Protein detection
automation, 2-D electrophoresis gels 133
Protein folding
simulation model, BPTI 243
Protein sequence
artificial neural networks, statistics 671
hydrophobic cluster analysis, MANSEK, SUNHCA 37
multi-profile plot, MacP12 760
oligopeptide frequency analysis, functional sites, domain localization 17
parallel computer, Profilesearch 25
Protein structure
databank, OMEGA 667
motif, Greek key jellyroll 709
Radioactive tracer
simulation, flux rate estimation in metabolic systems 573

Random
pattern distribution, RC-measure, JOINTD 275
Randomization
Windows 45
RC-measure
pattern distribution for random sequence, JOINTD 275
3-D reconstruction
electron microscopy, Fourier analysis, FT3D 681
Representation techniques
carbohydrate sequence analysis 723
RNA
3-D pencil models 465
display of secondary structure 551
tRNA
secondary structure folding, simulation 253
RNA sequence
phylogeny, Macintosh Hypercard 473
RNA structure
3-D modelling, 3DVISION 472
RSVP
sequence analysis using PostScript 421
Sample size estimation
Windows 45
SCAMP
metabolic pathway simulation 441
SCANGRAPH
TIFF file image scanning, graphical analysis 531
SCUM
cyanobacteria, bloom simulation 413
Secondary structure
DCSE 735
folding simulation, tRNA 253
RNA, graphics 551
prediction, ANTHEPROT 87
Sequence
amino acid, oligonucleotide primer design 469
splice site analysis, nucleic acid 617
Sequence alignment
multiple, C-DAC parallel computer 397
multiple, parallel simulated annealing 267
multiple 361
multiple from pairwise 169
pairwise, conserved regions 387
protein, CEDIT 741
protein, ENVIRON 639
protein, Pro Anal 491
protein, residue conservation, AMAS 745
protein, Smith–Waterman 729
secondary structure, DCSE 735
steady, similarity and distance 285
Sequence analysis
carbohydrate representation techniques 723
DNA footprinting, pattern recognition, DNA-Lexemics 349
FISH, GenBank 337
GSP 221
HYGCG 211
motif compliance, MOTIF 65
multiple alignment, secondary structure prediction, motif scanning, ANTHEPROT 87
nucleic acids, correlation image 331
nucleic acid, UNIREP 355
oligonucleotide database, ODS 427
pattern matching, ANREP 299
software package, PCAB 201
using PostScript, RSVP 421
weight array method 499
word recognition, PESTry 343
Sequence classification
homology, protein 205
Sequence databank
CD-ROM based query system, EMBL-Search 71
flat file library cross-referencing 59
Needleman–Wunsch, parallel computer 117
Sequence search
FASTPAT 541
SIGNAL SCAN 3.0
transcription factor binding site, database 113
SIMD
DNA sequence analysis, parallel computing 701
Simulation
crop selection 597
metabolic pathway, SCAMP 441
radioactive tracer, flux rate estimation 573
Simulation model
protein folding, BPTI 243
SITEVIDEO
nucleic acid sequence splice site analysis 617
Smith–Waterman
optimal protein sequence alignment 729
Splice site analysis
SITEVIDEO 617
Spreadsheet
curve fitting, error analysis, binding constants 127
SRS
flat file database retrieval tool, ODD language 49
STADEERS
biochemical engineering experimental design, BASIC 629
Statistical power analysis
Windows 45
Strain typing
microbial isolates, GROUP REP 403
String alignment algorithm
macromolecules, minimum message length 1
Structural motifs
protein, detection of 153
Structure
3-D pencil models, RNA 465
3-D structure
protein, sequence alignment 639
Structure analysis
curved DNA 435
protein, PACADE 259
SUNHCA
protein sequence, hydrophobic cluster analysis 37
SWISS-PROT
domain homology, FASTA search 371
Transcription control
oligonucleotide, vertebrate 647
Transcription factor
binding site, SIGNAL SCAN 3.0 113
TREECON
construction of evolutionary trees, software package 177
UNIREP
nucleic acid sequence analsyis 355
UNIX
biocomputing retrieval software, HYBROW 581
Fourier analysis, 3-D reconstruction 681
Vaccine design
monoclonal antibodies, genetic distance 101
VAX/Alpha
protein sequence analysis, BlockSearch 587
Weight array method
signal sequence analysis 499

Windows
sample size estimation, statistical power analysis 45
Word recognition
sequence analysis, PESTry 343
WORDUP
DNA sequence analysis, parallel computing 701
X-window
graphical user interface, GeneView 459
XE1D
electrophoregram analysis 451